

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 27, 2003, 08:52:11 ; Search time 43 Seconds

(without alignments)
991.901 Million cell updates/sec

Title: US-09-836-960-5

Perfect score: 1097
Sequence: 1 MYSAPSACTCICLHFLLCF.....PKYTTVTKRSRRIRTPHPA 207

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL_21:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.rvitus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1042	95.0	207	13	091950 gallus gall
2	363	53.1	210	13	057341 brachydanto
3	578	52.7	208	13	090XQ4 ambystoma m
4	578	52.7	212	13	09DE51 ambystoma m
5	576	52.5	210	13	042278 brachydanto
6	574	52.3	204	13	090696 gallus gall
7	556.5	50.7	200	13	P79925 xenopus lae
8	520.5	47.4	182	13	09PT78 oryzias lat
9	406	37.0	181	13	090Y80 lampetra ja
10	292	26.6	82	6	062682 canis fami
11	244	22.2	86	13	P79685 ambystoma m
12	234	21.3	80	13	090XQ0 ambystoma m
13	197.5	18.0	350	5	095YK8 clona savig
14	181	16.5	208	13	09PVY1 xenopus lae
15	177	16.1	186	6	095147 mustela vis
16	173	15.8	185	11	09ERN5 rattus norv

17	171	15.6	191	13	09DFC9	09dfc9 brachydanto
18	171	15.6	208	6	095112	095112 sus scrofa
19	164	14.9	212	11	09EST9	09est9 rattus norv
20	163.5	14.9	124	13	090XQ5	090xq5 ambystoma m
21	163.5	14.9	207	11	09ER05	09erq5 mus musculu
22	163	14.9	212	11	09ESL9	09esl9 mus musculu
23	162	14.8	208	6	095K97	095k97 macaca fasc
24	160.5	14.6	196	13	09YH31	09yh31 notophthalm
25	160.5	14.6	207	11	09ESL8	09esl8 mus musculu
26	159	14.5	195	11	08R5L6	08r5l6 rattus norv
27	158.5	14.4	130	6	077767	077767 canis fami
28	157	14.3	208	4	096P59	096p59 homo sapien
29	155.5	14.2	155	13	080P89	08gfr9 fuqu rubrip
30	153.5	14.0	213	6	09N1B9	09n1b9 ovis aries
31	153	13.9	108	6	09N1S7	09n1s7 capreolus c
32	153	13.9	192	11	09ERW3	09erw3 rattus norv
33	153	13.9	245	11	08VCY9	08vcy9 mus musculu
34	153	13.9	245	13	09W6A2	09w6a2 gallus gall
35	151.5	13.8	206	13	09YGD8	09ygd8 oncorhynch
36	151.5	13.8	212	13	042407	042407 gallus gall
37	151	13.8	153	11	0925A3	0925a3 mus musculu
38	150.5	13.7	155	13	090Y92	090y92 cynops pyrr
39	150	13.7	199	13	091A13	091a13 gallus gall
40	149.5	13.6	125	13	098TD8	098td8 cynops pyrr
41	148.5	13.5	111	13	090XQ1	090xq1 ambystoma m
42	147	13.5	301	5	08TRA3	08tra3 clona savig
43	147	13.4	208	11	08R5L5	08r5l5 rattus norv
44	146.5	13.4	196	4	P78443	P78443 homo sapien
45	145.5	13.3	106	6	09N1S8	09n1s8 capreolus c

ALIGNMENTS

RESULT 1
ID 091950 PRELIMINARY: PRT: 207 AA.

AC 091950;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FGF-18.
GN FGF-18.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-20368156; PubMed-10906450;
RA Ohuchi H., Kimura S., Watanabe M., Itoh N.;
RT "Involvement of fibroblast growth factor (FGF)18-FGF8 signaling in
RT specification of left-right asymmetry and brain and limb development
RT of the chick embryo";
RL Mech. Dev. 95:55-66(2000).
DR EMBL; AB030229; BAB9537.1; -.
DR HSSP; P3137L; IG82.
DR InterPro; IPR002209; HB/F-growthfact.
DR InterPro; IPR002348; IL1_HBGF.
DR Pfam; PF00167; FGF; 1.
DR PRINTS; PRO0262; IL1HBGF.
DR PROdom; PD000831; HB/F-growthfact; 1.
DR SMART; SM00442; FGF; 1.
DR PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ SPROUCE 207 AA; 24052 MW; 1DB6C82P2F26CC1 CRC64;

Query Match 95.0%; Score 1042; DB 13; Length 207;
Best Local Similarity 94.2%; Pred. No. 2e-87;
Matches 195; Conservative 8; Mismatches 4; Indels 0; Gaps 0;
QY 1 MYSAPSACTCICLHFLLCFQVOVLAEENVDFRIHENOTRRADVSRKQLRYOYSR 60
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Db      1  MSLSACTCLHLLFCQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSR 60
Oy      61  TSGKHIOVLGRISARGEDGDKYAQLLVETDFGSOVRIGKEFEFLCMNRKGLVGR 120
        61  TSGKHIOVLGRISARGEDGDKYAQLLVETDFGSOVRIGKEFEFLCMNRKGLVGR 120
Db      121  DGTSGKECVFIEKVLNNYALMSAKYSGWYGFTRKGRPRKGPRTRENODVHFMRYPK 180
        121  DGTSGKECVFIEKVLNNYALMSAKYSGWYGFTRKGRPRKGPRTRENODVHFMRYPK 180
Oy      181  GOPELOKPEKTYTTRKSRIRPTHPA 207
        181  GOPELOKPEKTYTTRKSRIRPTHPA 207
Db      181  GOPELOKPEKTYTTRKSRIRPTHPA 207
        181  GOPELOKPEKTYTTRKSRIRPTHPA 207

RESULT 2
057341
ID      057341      PRELIMINARY:      PRT:      210 AA.
AC      057341.
DT      01-JUN-1998 (TREMBlrel. 06, Created)
DT      01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Fibroblast growth factor 8.
GN      FGF8 OR FGF-8 OR FGF8.
OS      Brachydanio rerio (Zebrafish) (Zebra danio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_Taxid=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96043861; PubMed=9334274;
RA      Fuentehauer M., Thisse C., Thisse B.;
RT      "A role for FGF-8 in the dorsoventral patterning of the zebrafish
RT      gastrula.";
RL      Development 124:4253-4264(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96274197; PubMed=9609821;
RA      Reifers F., Boehl H., Walsh E.C., Crossley P.H., Stanier D.Y.R.,
RA      Brand M.;
RT      "Fgf8 is mutated in zebrafish acerebellar (ace) mutants and is
RT      required for maintenance of midbrain-hindbrain boundary development
RT      and somitogenesis.";
RL      Development 125:2381-2395(1998).
DR      EMBL; AF034264; AAC60303.1; -
DR      EMBL; AF051365; AAC41302.1; -
DR      HSSP; P31371; 1G82.
DR      ZFIN; ZDB-GENE-990415-72; fgf8.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      Pfam; PF00167; FGF; 1.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      SMART; SM00442; FGF; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
SQ      SEQUENCE 210 AA; 24697 MW; 9D9CA5B8E18A435A CRC64;

Query Match      53.1%; Score 583; DB 13; Length 210;
Best Local Similarity 55.9%; Pred. No. 1.7e-45;
Matches 113; Conservative 33; Mismatches 48; Indels 8; Gaps 4;
Oy      5  PSACICLHLLFCQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSRTSG 64
        5  PSACICLHLLFCQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSRTSG 64
Db      5  PSRLSYLHLHLFAFCYVAVVT-QSPNPTQHVSEOSKVTVSRRLIRTYOLYSRTSG 63
        5  PSRLSYLHLHLFAFCYVAVVT-QSPNPTQHVSEOSKVTVSRRLIRTYOLYSRTSG 63
Oy      65  HIOVL-GRISARGEDGDKYAQLLVETDFGSOVRIGKEFEFLCMNRKGLVGRPGT 123
        65  HIOVL-GRISARGEDGDKYAQLLVETDFGSOVRIGKEFEFLCMNRKGLVGRPGT 123
Db      64  HVOVLANKINAMADGVDHAKLIVETDFGSRVRIKGAETGFCYCMNRKGLVGRKGL 123
        64  HVOVLANKINAMADGVDHAKLIVETDFGSRVRIKGAETGFCYCMNRKGLVGRKGL 123
Oy      124  SKCEVIEKVLNNYALMSAKYSGWYGFTRKGRPRKGPRTRENODVHFMRYPK-Q 182
        124  SKCEVIEKVLNNYALMSAKYSGWYGFTRKGRPRKGPRTRENODVHFMRYPK-Q 182
Db      124  GKDCIFTEIVLNNYALONKYEGWYAFTRKGRPRKGSKTROHOREVHFMRKRLPKGH 183
        124  GKDCIFTEIVLNNYALONKYEGWYAFTRKGRPRKGSKTROHOREVHFMRKRLPKGH 183
Oy      183  PELOKPEKTYTTRKSRIRPTHPA 207
        183  PELOKPEKTYTTRKSRIRPTHPA 207

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Db      184  IAEHRPDEFINFPNRRTRR 205
        184  IAEHRPDEFINFPNRRTRR 205

RESULT 3
090X04
ID      090X04      PRELIMINARY:      PRT:      208 AA.
AC      090X04.
DT      01-DEC-2001 (TREMBlrel. 19, Created)
DT      01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Fibroblast growth factor 8 (Fragment).
OS      Ambystoma mexicanum (Axolotl).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC      Ambystoma.
OX      NCBI_Taxid=8296;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=21439472; PubMed=11555861;
RA      Christensen R.N., Weinstein M., Tassava R.A.;
RT      "Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning
RT      and semi-quantitative RT-PCR expression studies.";
RL      J. Exp. Zool. 290:529-540(2001).
DR      EMBL; AF360985; AAL16958.1; -
DR      InterPro; IPR002209; HB/F_growthfact.
DR      Pfam; PF00167; FGF; 1.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT      NON_TER      1
FT      NON_TER      1
FT      NON_TER      1
SQ      SEQUENCE 208 AA; 23977 MW; 9D32A77442AB070E CRC64;

Query Match      52.7%; Score 578; DB 13; Length 208;
Best Local Similarity 55.4%; Pred. No. 4.9e-45;
Matches 112; Conservative 34; Mismatches 50; Indels 6; Gaps 3;
Oy      4  APSACTCLHLLFCQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSRTSG 63
        4  APSACTCLHLLFCQVOMVAEENVDRIHVENOTRARDVSRKOLRYOLYSRTSG 63
Db      7  ASSVGYLLHLHLFLVCMQAKTV-QSPNPTQHVSRQSLVTDQLSRRLIRTYOLYSRPSG 65
        7  ASSVGYLLHLHLFLVCMQAKTV-QSPNPTQHVSRQSLVTDQLSRRLIRTYOLYSRPSG 65
Oy      64  KHIOVL-GRISARGEDGDKYAQLLVETDFGSOVRIGKEFEFLCMNRKGLVGRPG 122
        64  KHIOVL-GRISARGEDGDKYAQLLVETDFGSOVRIGKEFEFLCMNRKGLVGRPG 122
Db      66  KHVOVLANKINAMADGVDGSHAKLIVETDFGSRVRIKGAETGYTCMNRKGLVGRKGL 125
        66  KHVOVLANKINAMADGVDGSHAKLIVETDFGSRVRIKGAETGYTCMNRKGLVGRKGL 125
Oy      123  TSGKECVFIEKVLNNYALMSAKYSGWYGFTRKGRPRKGPRTRENODVHFMRYPK-G 181
        123  TSGKECVFIEKVLNNYALMSAKYSGWYGFTRKGRPRKGPRTRENODVHFMRYPK-G 181
Db      126  RKDCVFSFTVLENNYALONKYEGWYAFTRKGRPRKGSKTROHOREVHFMRKRLPKGH 185
        126  RKDCVFSFTVLENNYALONKYEGWYAFTRKGRPRKGSKTROHOREVHFMRKRLPKGH 185
Oy      182  --OPELOKPEKTYTTRKSRIR 200
        182  --OPELOKPEKTYTTRKSRIR 200
Db      186  OTTEPHRRPEFVNPFRNRKR 207
        186  OTTEPHRRPEFVNPFRNRKR 207

RESULT 4
09DE51
ID      09DE51      PRELIMINARY:      PRT:      212 AA.
AC      09DE51.
DT      01-MAR-2001 (TREMBlrel. 16, Created)
DT      01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT      01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE      Fibroblast growth factor 8.
GN      FGF-8.
OS      Ambystoma mexicanum (Axolotl).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC      Ambystoma.
OX      NCBI_Taxid=8296;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      Han M.J., Chung H.M., Nham S.U., Kim W.S.;
RT      "Partial cloning of FGF-8 cDNA in Mexican axolotl, Ambystoma
RT      mexicanum.";

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Query Match	52.5%;	Score 576;	DB 13;	Length 210;
Best Local Similarity	55.0%;	Pred. No. 7.6e-45;		
Matches 111;	Conservative 34;	Mismatches 49;	Indels 8;	Gaps 4;

RESULT 7
P79925

RESULT 7

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ID      P79925      PRELIMINARY;      PRT;      200 AA.
AC      P79925;
DT      01-MAY-1997 (TREMBLrel. 03, Created)
DT      01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Fibroblast growth factor 8 (Fragment).
GN      FGF-8.
OS      Xenopus laevis (African clawed frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC      Xenopodinae; Xenopus.
OX      NCBI_TaxID=8355;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98104248; Pubmed=9441681;
RA      Christen B., Slack J.M.W.;
RT      "FGF-8 is Associated with Anteroposterior Patterning and Limb
RT      Regeneration in Xenopus."
RL      Dev. Biol. 192:455-466(1997).
DR      EMBL; Y10312; CAA71365.1; -.
DR      HSSP; P31371; 1G82.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      InterPro; IPR002348; IL1_HBGF.
DR      Pfam; PF00167; FGF; 1.
DR      PRINTS; PR00262; IL1HBGF.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      SMART; SM00442; FGF; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT      NON_TER      200
FT      NON_TER      200
SQ      SEQUENCE      200 AA; 23453 MM; AB36B51C5ED5C7A CRC64;

Query Match      50.7%; Score 556.5; DB 13; Length 200;
Best Local Similarity 53.8%; Pred. No. 4.3e-43;
Matches 106; Conservative 34; Mismatches 40; Indels 17; Gaps 4;

QY      11 LCILHFLLCFQVQVVLVEENVDFRIHYENOTRRADDPVRSKOLRLYOLYSRTSGKHIOVL- 69
DB      11 LILHLFVYICQAO-----HYRQSLVTDLSRLIRLYOLYSRTSGKHVILA 58
QY      70 GRRISARGEDGKYAQLLVETDFGSOVRIKGETEFYLCMNRKGLVGPDKTSKECVF 129
DB      59 NKRINMAEDGDPAKLIVETDFGSRVRIKGAETGYICMNRKGLIGTNGKDCVF 118
QY      130 IEVLENNYATLMSAKSSGYVGFTRKGRPKRPTRENOODVHFMRKRYKQ--PELQK 167
DB      119 SEVLENNYATLVNVEGFMFTRGRPRKSGKTRQHOEVHFMRKLPKHHTEPHK 178
QY      188 PFKYTT--VTKRSRIR 202
DB      179 RFEFINVPRVRSKRTR 195

RESULT 8
ID      09PT78      PRELIMINARY;      PRT;      182 AA.
AC      09PT78;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Fgf8 (Fragment).
OS      Oryzias latipes (Medaka fish).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC      Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
OC      Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
OX      NCBI_TaxID=8090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Carl M., Wiltzprod J.;
RT      "Graded interference with FGF-signaling uncovers its dorso-ventral
RT      asymmetry at the mid-hindbrain boundary."
RT      Submitted (JUN-1999) to the EMBL/Genbank/DDJ databases.
EMBL; AJ243210; CAB64349.1; -.
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DR      HSSP; P31371; 1G82.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      InterPro; IPR002348; IL1_HBGF.
DR      Pfam; PF00167; FGF; 1.
DR      PRINTS; PR00262; IL1HBGF.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      SMART; SM00442; FGF; 1.
FT      NON_TER      1
FT      NON_TER      182
SQ      SEQUENCE      182 AA; 20702 MM; 1EF82473824A8DOC CRC64;

Query Match      47.4%; Score 520.5; DB 13; Length 182;
Best Local Similarity 62.8%; Pred. No. 7.5e-40;
Matches 93; Conservative 30; Mismatches 24; Indels 1; Gaps 1;

QY      36 HVENQTPARDDVRSKOLRLYOLYSRTSGKHIOVL-GRRISARGEDGKYAQLLVETDFG 94
DB      2 HVRQSVYTDVHSRRLRYOLYSRTSGKHVQVLSNKRINAMAEQVHAKLIVETDFG 61
QY      95 SOVRIRKGETEFYLCMNRKGLVGPDKTSKECVTEFKVLENNYATLMSAKSGYVGF 154
DB      62 SOVRIRKGAQGLYICMNRKGLIGTNGKQSRACIFTEIVLENNYATLRNHYNDWYMAFT 121
QY      155 KKGPRKGPRTRENOODVHFMRKRYKQ 182
DB      122 RRGPRKGSQTRQHOEVHFMRKRLPRQ 149

RESULT 9
ID      090Y80      PRELIMINARY;      PRT;      181 AA.
AC      090Y80;
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE      01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE      Ljfgf8 (Fragment).
GN      Ljfgf8.
OS      Lampetra japonica (Japanese lamprey) (Entosphenus japonicus).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
OC      Petromyzontiformes; Petromyzontidae; Lethenteron.
OX      NCBI_TaxID=94989;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Shigetani Y., Sugahara F., Kawakami Y., Hirano S.,
RA      Kuratani S.;
RT      "Shape precedes structure: an exaptation for the vertebrate jaw
RT      evolution."
RL      Submitted (SEP-2001) to the EMBL/Genbank/DDJ databases.
DR      EMBL; AB071892; BAB68397.1; -.
DR      InterPro; IPR002209; HB/F_growthfact.
DR      Pfam; PF00167; FGF; 1.
DR      ProDom; PD000831; HB/F_growthfact; 1.
DR      PROSITE; PS00247; HBGF_FGF; UNKNOWN_1.
FT      NON_TER      1
FT      NON_TER      181
SQ      SEQUENCE      181 AA; 20920 MM; 8F40A6764CE663DC CRC64;

Query Match      37.0%; Score 406; DB 13; Length 181;
Best Local Similarity 57.7%; Pred. No. 2.2e-29;
Matches 75; Conservative 25; Mismatches 28; Indels 2; Gaps 1;

QY      74 SARGEDGDKYAOQLLVETDFGSOVRIKGETEFYLCMNRKGLVGPDKTSKECVTEFK 133
DB      1 NARADGDNKFAKLIVETDFGSRVRIKGAESGYICMNRKGLVGPDKTSKECVTEFK 60
QY      134 LENNYATLMSAKSGYVGFTRKGRPKRPTRENOODVHFMRKRYKGPPELQKPF--KY 191
DB      61 LENNYATLMSVNGWYMGFTGRGRKSGTSQHOEVHFMRKRPQRTSEERERKFIQVA 120
QY      192 TTYTKRSRRI 201
DB      121 TGAARSKRM 130
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[illegible]

QY	127	CVFIEIKVLENNYTA	LSAKSYGSGWYGFTRKGRGPKTR	ENOQDVHEMKRYPKG---	Q 182
Db	2	CVFSEVIEENNTALQ	NKYEGMWMAFTRGPRRGSKTRQ	HOREVHEMKRYPKG	61
QY	183	PELOKPFKTYT	TKRSRIRPTHP	206	
Db	62	PHRREFVNP	PNRKRSHSV	85	
RESULT 12					
ID	Q90X00	PRELIMINARY:	PRT:	80 AA.	
AC	Q90X00:				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21, last annotation update)			
DE	Fibroblast growth factor 8 (Fragment).				
OS	Ambystoma maculatum (spotted salamander).				
OC	Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,				
CC	Amphibia, Batrachia, Caudata, Salamandroidea, Ambystomatidae,				
CC	Ambystoma.				
OX	NCBI_TaxID=43114;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21439472; PubMed=11555861;				
RA	Christensen R.N., Weinstein M., Tassava R.A.;				
RT	"Fibroblast growth factors in regenerating limbs of Ambystoma: Cloning and semi-quantitative RT-PCR expression studies.";				
RL	J. Exp. Zool. 290:529-540(2001).				
DR	EMBL; AF360989; AAL16962.1; "				
DR	InterPro: IPR002209; HB/F_growthfact.				
PF	Pfam: PF00167; FGF: 1.				
DR	Prodom: PD000831; HB/F_growthfact. 1.				
FT	NON_TER	1			
FT	NON_TER	80			
FT	NON_TER	80			
SO	SEQUENCE	80 AA; 9689 MW; 16A5FD6A193F5779 CRC64;			
Query Match 21.3%; Score 234; DB 13; Length 80;					
Best Local Similarity 57.7%; Pred. No. 4.2e-14;					
Matches 45; Conservative 11; Mismatches 18; Indels 4; Gaps 1;					
QY	127	CVFIEIKVLENNYTA	LSAKSYGSGWYGFTRKGRGPKTR <td>ENOQDVHEMKRYPKG---</td> <td>Q 182</td>	ENOQDVHEMKRYPKG---	Q 182
Db	2	CVFSEVIEENNTALQ	NKYEGMWMAFTRGPRRGSKTRQ	HOREVHEMKRYPKG	61
QY	183	PELOKPFKTYT	TKRSRIRPTHP	206	
Db	62	PHRREFVNP	PNRKRSHSV	85	
RESULT 13					
ID	Q95YK8	PRELIMINARY:	PRT:	350 AA.	
AC	Q95YK8:				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, last sequence update)			
DT	01-JUN-2002	(TREMBLrel. 21, last annotation update)			
DE	Fibroblast growth factor A.				
CS	CS-FGA.				
OS	Ciona savignyi.				
OC	Eukaryota, Metazoa, Chordata, Urochordata; Ascidiacea; Enterogona;				
CC	Phlebobranchia; Clonidae; Clona.				
OX	NCBI_TaxID=51511;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Satou Y., Imai K.S., Satoh N.;				
RT	"Ciona savignyi genes.";				
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AB057737; BAB68346.1; "				
DR	InterPro: IPR002209; HB/F_growthfact.				

